

FIG. 1A

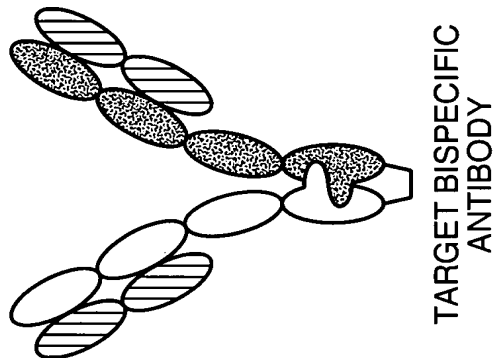


FIG. 1C

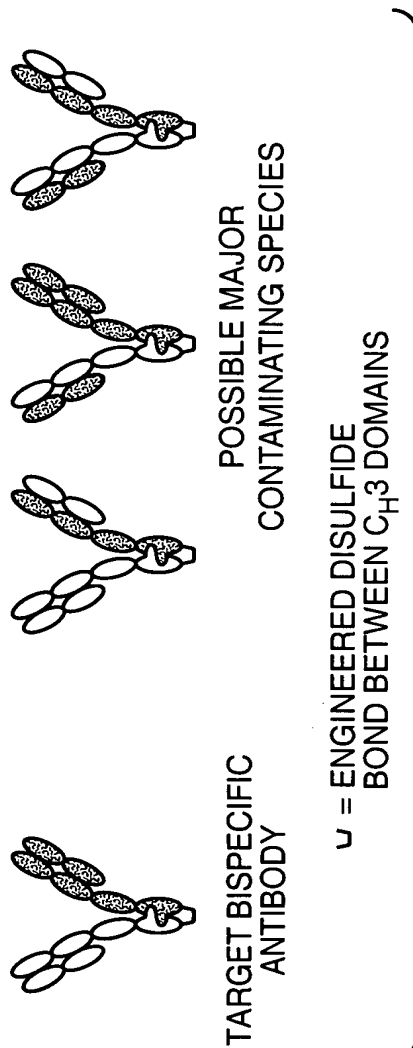


FIG. 1B

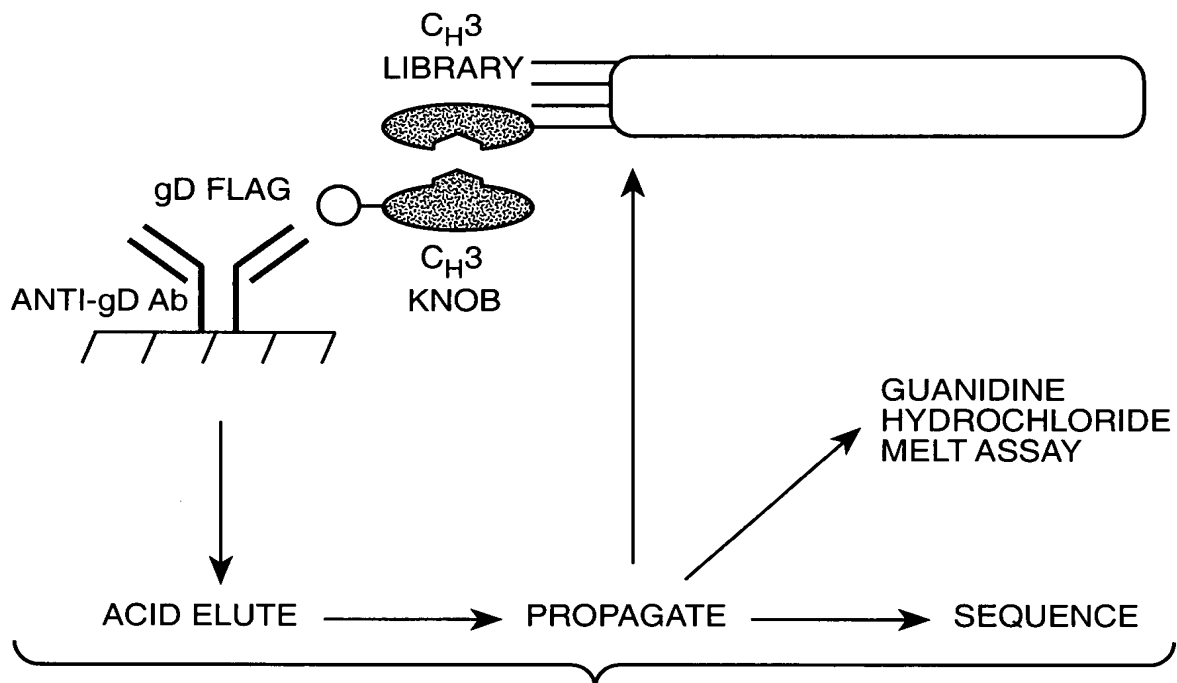


FIG. 2A



FIG. 2B

FIG. 2C-1

FIG. 2C-2

FIG. 2C

FIG. 2C-1

```
stII      -> gD flag      -> G site      -> CH3
N A Y A L K M A D P N R F R G K D L A A H Y G Q P
AACGCGTACGCTCTGAAAAATGGCGGACCCGAAACCGTTTTCGTGGTAAAGATCTGGCTGCACACTACGGCCAGCCG
MluI      75
R E P Q V Y T L P P S R E E M T K N Q V S L W C L
CGGGAACCTCAGGTGTATACCTGCCACCGTCTCGAGAAAGAAATGACTAAAAACCAAGGTCTCTCTGTGGTGCCTG
150
V K G F Y P S D I A V E W E S N G Q P E N N Y K T
GTCAAAGGTTTCTATCCGAGCGATATCGCCCGTGGAAATGGGAAAGCAACGGTCAACCCGGAAAAACAACACTACAAAACC
225
T P P V L D S D G S F F L Y S K L T V D K S R W Q
ACTCCACCGGTGCTGATTCTGTATGGCTCCTTCTTCTGTATTTCGAAGCTGACCGTTGACAAAAGCCGTTGGCAG
300
```

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420                               430                               440
Q G N V F S C S V M H E A L M N H Y T Q K S L S L
CAAGGCAACGTTTTCAGCTGTTCTGTTATGCACGAGGCCCTTGACAAACCACCTACACCCAGAAAAGCCTGTCCCTG
375
S P G K O                               M K K N I A F L L
TCTCCCCGGGAAATAAGCTGAGGCTCCTCTAGAGGTTGAGGTGATTTATGAAAAAGAAATATCGCATTTCTTCTTG
450
-> stII
A S M F V F S I A T N A Y A G Q P R E P Q V Y T L
350
CATCTATGTTTCGTTTTCATGCTACAAACGCGTACGCTGGGAGCCCGAGAACCCACAGGTGTACACCCCTGC
525
-> CH3
P P S R E E M T K N Q V S L Y C L V K G F Y P S D
360 366 368 370
CCCCATCCCGGAAGAGATGACCAAGAACCAGGTAAGCTTGTAAGCTTGGTCAAGGCTTCTATCCCAGCGACA
600
HindIII
I A V E W E S N G Q P E N N Y K T T P P V L D S D
380 390 400
TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGGTGGACTCCGACG
675
                               410                               420
G S F F L Y S F L T V D K S R W Q Q G N V F S C S
GTCCTTCTCCTCTACAGCTTTCACCGTCGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCTCATGCTCCG
750
SalI
V M H E A L H N H Y T Q K S L S L S P G K Am G P
430 440
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAGAGCCCTCTCCCTGTCTCCGGGTAATAGGGGCC (SEQ ID NO: 13)
ApaI
```

FIG. 2C-2

Ab T366W, Ia T366S:L368A:Y407V

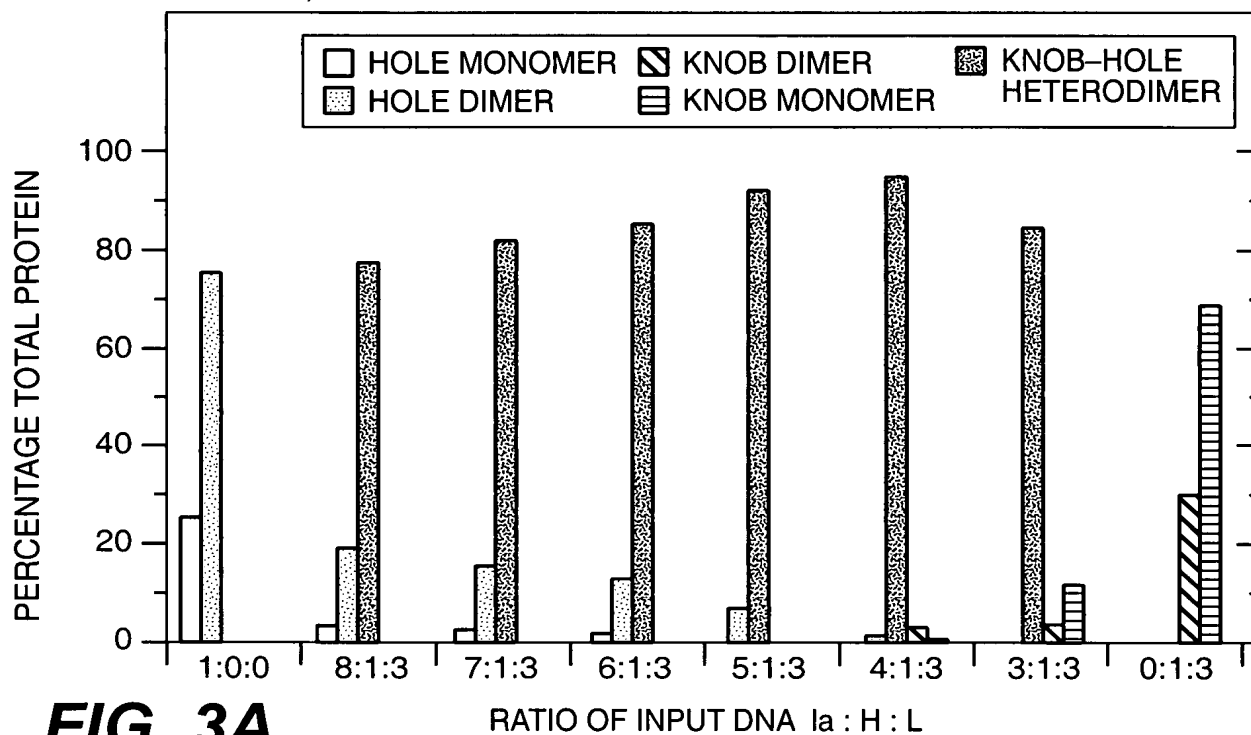


FIG. 3A

Ab T366W, Ia Y407A

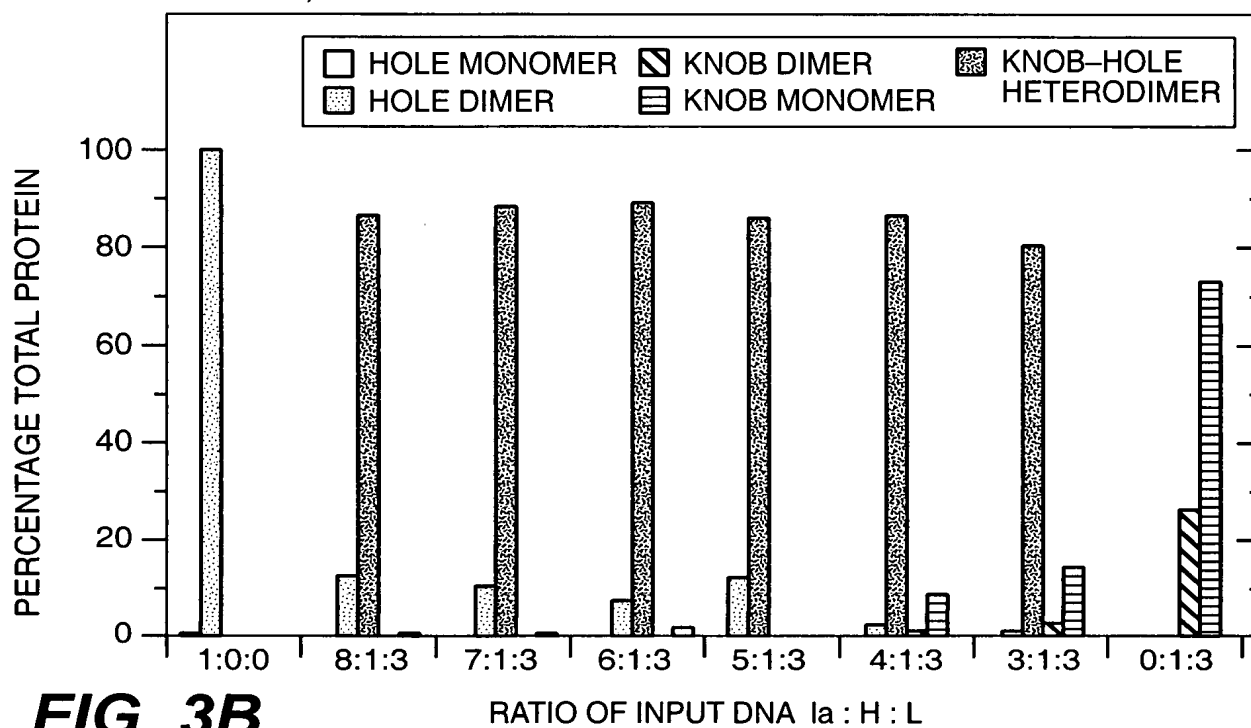
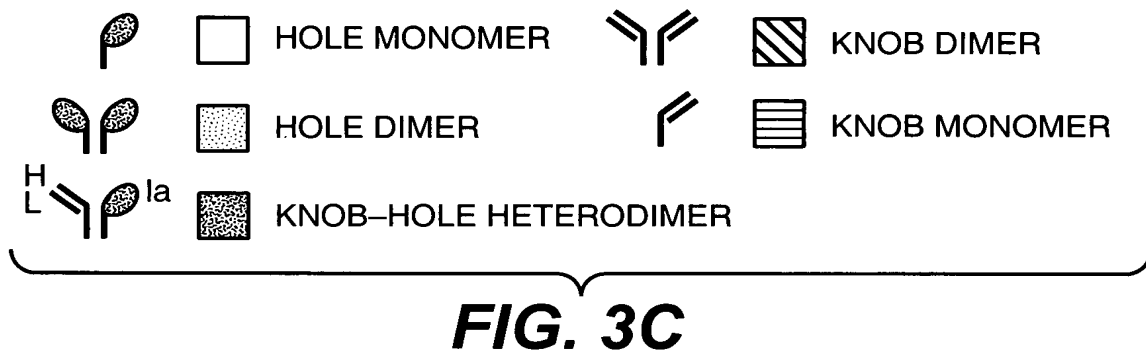


FIG. 3B



	1	20	abc	30	40	50	
Ax1.78	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
Rse.23	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
IgER.MAT2C1G11	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
GCSFR.A4	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
Rse.04	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
obr.4	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
Rse.20	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
Rse.15	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
veg.f.5	QSVLTQPA	SVSGSPGQ	SITISCTGT	SSDVGGY	NYVSWY	QQHPGKAPK	LMIEGSKRPSGV
		#####				###	
			CDR L1				CDR L2
	60	70	80	90	a	100	
Ax1.78	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 14)
Rse.23	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 15)
IgER.MAT2C1G11	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 16)
GCSFR.A4	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 17)
Rse.04	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 18)
obr.4	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 19)
Rse.20	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 20)
Rse.15	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 21)
veg.f.5	SNRFSGSK	SGNTASLT	ISGLQAE	DEADY	CSSY	TRSTRV	FGGTKLTVL (SEQ ID NO: 22)
			#####			###	
							CDR L3

FIG. 4

FIG. 5

	H1	H2	H3	H4	H5	H6	H7	H8	H9	H10	H11
O1	49	47	51	81	60	48	76	51	100	62	51
O2	84	79	88	50	48	99	48	88	48	45	88
O3	83	82	85	51	50	95	49	85	49	46	85
O4	47	50	51	83	77	48	65	51	73	64	51
O5	49	47	51	81	60	48	76	51	100	62	51
O6	83	79	86	50	50	99	47	86	48	45	86
O7	81	100	86	51	49	80	48	86	47	44	86
O8	81	100	86	51	49	80	48	86	47	44	86
O9	81	100	86	51	49	80	48	86	47	44	86
O10	83	79	85	50	49	98	46	85	48	45	85
O11	83	80	87	50	49	99	47	87	48	45	87
O12	81	100	86	51	49	80	48	86	47	44	86
O13	49	47	51	81	60	48	76	51	100	62	51
O14	50	50	54	95	67	49	76	54	75	62	54
O15	82	79	85	49	48	97	46	85	47	44	85
O16	84	80	87	50	49	100	47	87	48	45	87
O17	45	44	47	65	62	45	62	47	62	100	47
O18	50	51	50	75	79	50	63	50	66	62	50

O1-O18: ANTI-Ob-R ANTIBODY CLONES obr. 1, 11, 12, 14, 15, 16, 17, 18, 19, 2, 20, 21, 22, 23, 24, 26, 3, 4, RESPECTIVELY.

H1-H11: ANTI-HER3 ANTIBODY CLONES her3.1, 3.10, 3.11, 3.12, 3.16, 3.18, 3.19, 3.22, 3.3, 3.4, 3.7, RESPECTIVELY.

FIG. 6